

Presentation and Validation of an Accurate and Effective Segmentation for Dynamic Heart Modeling

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Abstract-An accurate and effective segmentation technique is the basis of the ideal dynamic heart modeling. In this paper, a novel multistage approach is proposed to perform the segmentation for the heart modeling and its multistage segmentation procedure orderly consists of four stages: Morphological Recursive Erosion (MRE); Fast Marching (FM); 3D Morphological Reconstruction (MR) and Morphological Recursive Dilation (MRD). To prove its accuracy and effectiveness, the approach is tested on 3 CT datasets of beating hearts with each set containing ten individual volumes throughout a cardiac cycle. In order to validate the segmentation results, a novel Radial Distance Based Validation (RDBV) method is also presented in this paper that provide the Global Accuracy (GA) measure to evaluate the segmentation accuracy. GA is calculated based on a Local Radial Distance Error (LRDE), which is along the radii emitted from the points along the skeleton of the object, to accommodate the complicated cardiac structure. The RDBV is improved in the universality and ability to reflect significant local errors in global accuracy function. The average accuracy of the proposed segmentation approach using the RDBV is 0.783.

I. INTRODUCTION

The physical characterization of the deformation of the whole heart volume is the fundamental step toward understanding the physiology of normal heart and the effects of cardiovascular disease. Besides, the deformation can provide rudiments of the surgical simulation of the heart [1]. Thus, the dynamic heart modeling that simulates the heart deformation is essential in the cardiac research and clinical application.

Segmentation technique plays an essential role in the heart modeling and affects the quantity of the modeling quality significantly.

Several segmentation algorithms on the heart can be found in the literatures. The Snake [2], introduced by Kass et al, provides a general model-based solution to the segmentation problem. As most common model-based methods, Level Set [3] methods solve region breaking and merging problems with an additional dimension. Watershed [4] and Morphological Reconstruction (MR) [5] are two main region-based methods and both derived from mathematical morphology. Since region-based methods are operated in each pixel, they are usually accurate, but limited in effectiveness.

Besides, many other novel model-based algorithms were proposed, such as [6][7]. However, most of them are focused only on extracting the left or right ventricular from cardiac image.

In this paper, we propose a multistage segmentation approach that integrates both the advantages of model-based methods and region-based methods to deal with the whole heart body.

In the segmentation research, validation is an essential part. Several validation methods had been proposed, such as Similarity Index (SI) [8], Relative Difference Degree (RDD) and Relative Overlap Degree (ROD) [9], et. al. However, Validation of segmentation methods is still an open question. There are still several challenges. This paper presents a novel radial distance based validation (RDBV) method that can evaluate the segmentation of all kinds of complicated structures including the heart. Its advantages over standard techniques such as SI are its universality and ability to reflect significant local errors in global accuracy function.

The rest of this paper is organized as follows: in section II, we introduce the multistage segmentation for dynamic heart modeling; section III describes the framework of the novel validation method -- RDBV; then we focus on the design of target function employed in RDBV in section IV; experimental results are give in section V.

II. MULTISTAGE SEGMENTAION ON HEARTS

A. Fast Marching and MR

The Fast Marching (FM) [10] algorithm is a special case of the level Set segmentation method. While the sign of the speed function in general in level set approaches can be both positive and negative, that in the FM algorithm does not change. This property makes it faster. Since the FM is based on a deforming front model, the propagating front line is designed to keep smooth during the deformation. If the object boundary is not smooth, the method can hardly match it perfectly, as shown in Fig.1 (a).



Fig. 1. Comparing the segmentation features of Fast Matching (a) with MR (b), where the black lines represent the object edge and the highlighted lines depict the segmented lines.

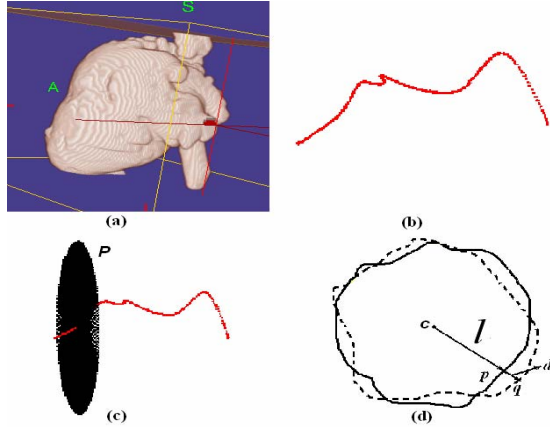


Fig. 2. Calculation of LRDE. (a) is the origin data of heart; (b) is the skeleton of (a) computed by distance mapping method; (c) shows the radial construction and (d) represents the computation of Local radial distance error (LRDE), where Certain radial l intersects with S (dotted curve) and G (real curve) resulting the intersection points q and p , respectively. d denotes the LRDE along l .

MR is a typical approach to extract seeded regions employing morphological operations. Since it is operated in individual pixels, MR can easily fit into the small sharp regions along the edge of ROI, as shown in Fig.1. (b). However, MR is time consuming to recover ROI from a user-defined initial seed.

Based on the main ideas of FM and MR described above, a novel multistage segmentation method is proposed.

B. Multistage Segmentation Strategy

This idea of the multistage segmentation can be implemented in four steps:

1) *Reduce the connectivity between region of heart and the neighboring tissues.* Recursively erode the input 3D heart image using a structuring element base (e.g. a sphere with 1 pixel radius) until the heart is completely separated from the neighboring tissues, as determined by the operator.

2) *Perform FM segmentation.* After connectivity reducing, the FM method is employed to initially propagate the user-defined seed to a position close to the boundary of heart and it performs rapidly.

3) *Implement 3D MR.* Taking the output of the improved FM as its seed, MR algorithm is employed to refine the seed to the a further result.

4) *Recover the lost data elements from the first stage.* During the recursive erosion in stage 1, part of the object is also often eliminated. To recover these lost components, the recursive dilation method is employed. The reconstructed heart surface is dilated recursively using the same number of iterations N as recorded in the first stage, which results in the recovery of the heart surface to the “original” position.

Employing the output of the improved FM as the initial seed, the MR process is much faster and remains its accuracy. Thus, we can make full use of the fast speed of the improved FM and the accuracy of the MR.

III. VALIDATION

A. Calculation of LRDE

As described in I, an ideal validation is still challenging. Besides the lack of acceptable gold standards, universality and robustness are the two main challenges:

1) *Universality:* Because of the complicated structure of the heart and its blood vessels, many existed validation methods are not fit for it. A more universal validation is needed.

2) *Robustness:* The more accurate the segmentation is, the better measure the validation method should result in. we will discuss it in section IV in detail.

In order to meet these two challenges, we propose a novel radial distance based validation (RDBV) method where the radii are extended from the points along the skeleton of the heart.

Several skeleton algorithms can be found in the literature. In this paper, we employ distance-mapping [11] method to extract the skeleton of the heart, shown in Fig.2 (b). Then, we construct the radii that extended from points along the skeleton.

Suppose that c is a point along the skeleton and P is the plane perpendicular to the skeleton in point c . Then, we construct sufficient equi-spaced radii in plane P . as shown in Fig.2 (c). Each radial line intersects the surfaces of the segmented region S and the corresponding ground truth image G . Taking one of the radial lines l for example, the intersection points are q and p , respectively (see Fig.2 (d)). $d = cq - cp$ is defined as the local radial distance error (LRDE) in the direction of l . Thereby, all the LRDE measures of the radii extended from c are calculated.

In the same way described above, all LRDE measures of radii extended form all points along the skeleton of the heart can be calculated easily.

In addition, due to the roughness of the original skeleton line, the proposed radial lines are distributed unevenly. To improve the situation, a B-Spline is used to smooth the skeleton line, and the LRDE are recalculated for uniform distribution over all areas of the surfaces of S and G .

B. Framework of RDBV

Points along the skeleton are numbered in order as $c_0, c_1, c_2 \dots c_{N-1}$, where N is the number of points. Furthermore, radial lines emitted from the point c_i are denoted $R_{i1}, R_{i2}, R_{i3} \dots R_{iM}$, where M is the number of radii emitted from c_i , and the intersection points on the surfaces S and G are presented as $q_{i0}, q_{i1}, q_{i2} \dots q_{iN}$ and $p_{i0}, p_{i1}, p_{i2} \dots p_{iM}$, respectively. Thus, we give the formal definition of LRDE:

$$d_{ij} = c_i q_{ij} - c_i p_{ij} \quad (0 \leq i < N, 0 \leq j < M) \quad (1)$$

Furthermore, the intermediate variable f_{ij} is defined as below:



Fig.3. Two typical segmentation results. In both (a) and (b), the black real lines stand for the contours of “gold stand”, while the red dashed lines denote the ones of the segmented results.

$$f_{ij} = \left| \frac{d_{ij}}{\varphi_i P_{ij}} \right| \quad (0 \leq i \leq N-1, 0 \leq j \leq M-1) \quad (2)$$

f_{ij} reflects the fractional under-segmentation or over-segmentation along the direction of R_{ij} . We place f_{ij} in one of three categories:

- $0 < f_{ij} \leq 1/k$: Local segmentation is considered accurate;
- $1/k < f_{ij} < 2/k$: Local segmentation is acceptable;
- $2/k \leq f_{ij}$: Local segmentation is unacceptable.

Based on statistic and the experienced radiologists' advices, $f_{ij} \leq 0.05$ is considered to present an accurate local segmentation, leading to the selection of a value of 20 for k as a constant defining an acceptable segmentation. Furthermore, we introduce the concept of Global Accuracy (GA) to reflect the accuracy of the global segmentation:

$$GA = NM \left[\sum_{i,j=0}^{N-1, M-1} L_{i,j} \right]^{-1} \quad (0 \leq i \leq N-1, 0 \leq j \leq M-1) \quad (3)$$

Where, the target function $L_{i,j}$ is defined as:

$$L_{ij} = \lambda^{f_{ij}k} \quad (0 \leq i \leq N-1, 0 \leq j \leq M-1) \quad (4)$$

And, $\lambda = 1.54$

We will discuss this target function and its coefficient λ in the following section.

Since $f_{ij} \leq 1/k$ is considered as an accurate segmentation, we can define GA_t , the threshold value of GA, as:

$$GA_t = NM \left[\sum_{i,j=0}^{N-1, M-1} \lambda^{\frac{1}{k}} \right]^{-1} = 0.65 \quad (0 \leq i \leq N-1, 0 \leq j \leq M-1) \quad (5)$$

So, $GA \geq GA_t = 0.65$ is considered to be a good segmentation when using the RDBV method.

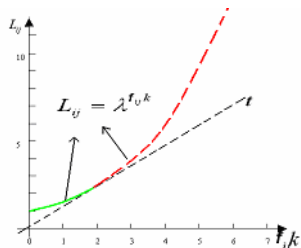


Fig. 4. Target Function L_{ij} ($k=20$). It is designed to penalize the significant inaccuracy in RDBV. The dashed line t has a unit slope.

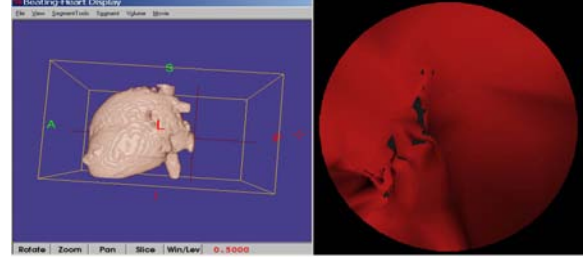


Fig. 5. The platform of the dynamic heart model; (a) A snapshot of the UI of the “Beating-Heart” software; (b) shows the heart endoscope integrated in the platform.

IV. TARGET FUNCTION

As shown in Fig.3, two different segmentation results are depicted. Although they result in almost same average distance error, the result shown in Fig.3 (a) is considered much better than that in (b). In another words, the result shown in Fig.3 (b) has significant local error that always reflects some import information, even though it is accurate in many other areas. However, many existing validation methods cannot distinguish between these two situations. In this paper, we propose GA as a novel criterion to accurately measure them.

In order to overcome the shortcoming described above, in GA we design a target function $L_{ij} = \lambda^{c_{ij}k}$ to penalize the significant local inaccuracy. Meanwhile, the conditions that target function should satisfy:

$$\begin{cases} \frac{dL_{ij}}{d(f_{ij}k)} < 1, & 0 \leq f_{ij} < \frac{2}{k} \\ \frac{dL_{ij}}{d(f_{ij}k)} = 1, & f_{ij} = \frac{2}{k} \\ \frac{dL_{ij}}{d(f_{ij}k)} > 1, & f_{ij} > \frac{2}{k} \end{cases} \quad (0 \leq i \leq N-1, 0 \leq j \leq M-1) \quad (6)$$

From $\frac{dL_{ij}}{d(f_{ij}k)} = 1, f_{ij} = \frac{2}{k}$, we get an equation in λ :

$$\ln \lambda \times \lambda^2 = 1 \quad (7)$$

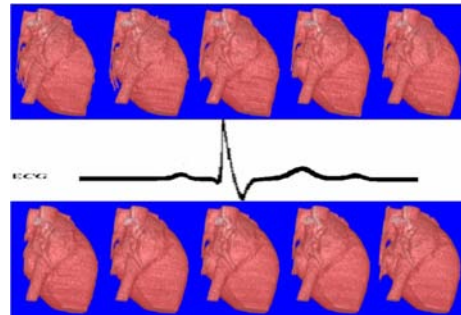


Fig. 6. Examples of segmentation results of hearts throughout the cardiac cycle.

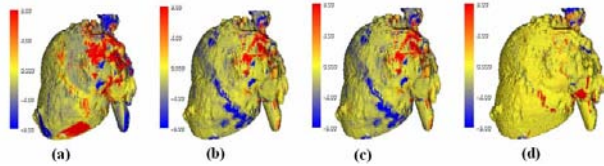


Fig. 7. Segmentation results of the FM (a), MR(b), Proposed Multistage Method (c) and Watershed (d) on hearts.

Solving (7) yields: $\lambda = 1.54$.

The characterization of this target function is described below:

- Local segmentation is regarded as accurate or acceptable. This corresponds to the target function L_{ij} being nearly flat (as shown as the real curve in Fig.4.).
- Local segmentation is regarded as unacceptable. The target function changes quickly with the increase of the combined variable c_{ijk} (as shown as the dotted curve in Fig.4.), penalizing the inaccuracy in the unacceptable region.

V. EXPERIMENTS

In order to construct the dynamic heat modeling, we developed the “Beating-Heart” software environment, which is based on VTK and Python language, shown in Fig 5. This environment also performs the segmentation and validation running on a Pentium IV 2.0 GHz CPU desktop computer with MS-windows XP operation system.

In our experiment, 3 series of CT canine heart volumes ($512 \times 512 \times 87$) were tested. The “ground truth” of each real clinical dataset was manually defined by an expert radiologist. Examples of segmented results using the proposed approach are shown in Fig.6.

In addition, The FM, MR, Watershed and the proposed multistage method are compared and evaluated with respect to both accuracy and efficiency using the RDBV metric. Fig.7., Table 1 and 2 reveal that the proposed multistage segmentation is superior to the other algorithms on the heart.

VI. CONCLUSION

In this paper, we presented a new multistage segmentation method on the heart. This method integrates both the advantages of FM and MR, and it is considered effective and accurate. Meanwhile, the RDBV method is proposed to offer an improved measure of the segmentation results using both local and global information.

As the future work, we will apply the proposed segmentation method and RDBV to more clinical application.

TABLE1
AVERAGE GLOBAL ACCURACY (GA) MEASURE OF FM, MR, PROPOSED MULTISTAGE METHOD (PMM) AND WATERSHED (WA) ON EACH DATASET OF HEATS

Datasets	FM	MR	PMM	WA
Dataset1	0.661	0.775	0.775	0.918
Dataset2	0.694	0.788	0.786	0.968
Dataset3	0.674	0.781	0.787	0.942
Average	0.677	0.781	0.783	0.943

TABLE2
AVERAGE COMPUTING TIME IN SECONDS OF FM, MR, PROPOSED MULTISTAGE METHOD (PMM) AND WATERSHED (WA) ON EACH DATASET OF HEATS

Datasets	FM	MR	PMM	WA
Dataset1	66.9	442.1	120.8	562.6
Dataset2	68.7	450.6	116.6	549.3
Dataset3	67.4	466.2	137.0	558.7

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